nucleotide polymorphism (SNP) discovered in the methylenetetrahydrofolate reductase (MTHFR) gene (Van der Put et al. 1998). We agree that the numbering that was used may be confusing for two reasons.

First, we designated this SNP as the "1298(A→C) mutation," by use of the same numbering method used to indicate the 677(C→T) substitution, the first SNP discovered in the MTHFR gene (Frosst et al. 1995). Although this SNP is designated to be at position 677, the actual location of this SNP may be at position 665 of the coding region, if numbering is started at the first ATG site of the reported coding sequence (Goyette et al. 1994). Thus, discrepancies in numbering started before the discovery of the second SNP. We therefore had two options for determining the nomenclature of the second SNP in the MTHFR gene: either to start numbering at the ATG or to use the method of numbering that is in concordance with that used for the first SNP. In our opinion, this last option would be more reasonable, because of the widely accepted nomenclature of the 677(C→T) substitution. Therefore, we designated the second SNP as the "1298(A→C) mutation."

Second, the sequence reported by Goyette et al. (1994) unfortunately contained a C at the 1298 sequence, instead of at the much more common 1298A sequence, of the MTHFR gene. We have no doubt that the mutation is an A→C, rather than a C→A, transition, which is clearly reflected by the prevalence of the 1298 SNP and its effect on MTHFR activity (van der Put et al. 1998).

Additionally, we would like to describe an improved method of PCR/RFLP screening for the 1298 SNP. By use of two PCR primers—forward primer ATGTGGGGGGAGGAGCTGAC and the intronic reverse primer GTCTCCCAACTTACCCTTCTCCC—a 241-bp fragment will be obtained. If the wild-type genotype (1298AA) is present, then the *Mbo*II RFLP results in two fragments—one that is 204 bp and one that is 37 bp. For the homozygous mutated MTHFR genotype (1298CC), only the 241-bp fragment is obtained, and, for the heterozygous genotype, all three fragments are obtained. These RFLP fragments can be easily differentiated by means of agarose-gel electrophoresis.

We examined the possible interference of the 1317(T→C) transition with the proper screening of the 1298 SNP. 1317(T→C) is a silent mutation (Weisberg et al. 1998) that, like the 1298 SNP, results in the formation of an *Mbo*II recognition site and that could thus disturb genotyping of 1298. We performed restriction-enzyme analysis with *Mbo*II and *Bpu*AI—the latter restriction enzyme recognizes only the 1317(T→C) substitution—on the PCR-obtained 241-bp fragment and looked for possible misinterpretation of the 1298 genotype. The 1317CC genotype was not observed among 450 Dutch individuals, and we observed only 3 heterozygous individuals, which resulted in the 1317C allele having a frequency of .003 among the Dutch population. The 1317 SNP did not interfere with the proper genotyping of 1298; in all three cases, the 1317C allele was present on a 1298A allele, which already results in a *Mbo*II recognition site. Possibly, the 1317C substitution arose at the 1298A allele and, thus, will not disturb genotyping of 1298.

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Special Oversight Groups to Add Protections for Population-Based Repository Samples

To the Editor:

The National Institute of General Medical Sciences (NIGMS) supports the Human Genetic Cell Repository through a contract to the Coriell Institute for Medical Research in Camden, NJ. The repository supplies cell lines and DNA samples to investigators worldwide. Al-

though most of the 6,300 cell lines in the repository are derived from individuals with genetic disorders or from their family members, others in the repository were acquired because they represent distinct, identified populations. Designated as the Human Variation Collection, these samples come from anonymous, unrelated individuals and have no phenotypic information associated with them. In recent years, researchers have shown a growing interest in studying these samples (1) to answer fundamental questions related to genetic architecture of complex traits, (2) to distinguish between a disease-causing mutation and a normal polymorphism, and (3) to identify genes in rare and common disorders. This interest has prompted the genetics research community to ask the repository to acquire samples from additional identified populations. At the same time, members of some populations and some bioethicists have raised concerns about possible negative consequences (such as stereotyping, stigmatization, discrimination, and community disruption) to a population resulting from genetic studies on identified populations.

NIGMS recently held a workshop (Workshop on Population-Based Samples for the NIGMS Human Genetic Cell Repository) to consider the scientific benefits and the risks to populations of expanding the collection of such samples and to develop recommendations about whether, and under what conditions, the repository should acquire these samples. A key set of recommendations describes a novel approach to increase the protection of populations, and it is the purpose of this letter both to inform the human genetics research community about these recommendations and to encourage further discussion about the means to protect populations in genetics research. In parallel, additional input from members of diverse populations is being sought.

Federal regulations (Title 45, Code of Federal Regulations, Part 46) focus on the protection of individuals and do not extend protections to populations or other groups. The recommendations of the Workshop on Population-Based Samples for the NIGMS Human Genetic Cell Repository were designed to complement the federal regulations by establishing an Oversight Group for Population-Based Samples (OGPBS) that would assure that samples were (or will be) acquired with due protection of the population from which samples are collected. As detailed in the report of the Workshop on Population-Based Samples for the NIGMS Human Genetic Cell Repository, each population-specific OGPBS would specify criteria for consultation with and participation by members of the population; for informing the population and individual sample donors about the use of the samples, the benefits, if any, that are promised, the potential harm to the population, and what will be done to minimize harm; and for the documentation about these activities required from investigators who collect samples for submission to the repository.

An alternative to the OGPBS model would be for institutional review boards (IRBs) to be more vigilant in their protection of populations. There are several advantages, however, to using an OGPBS for this purpose. First, it is unlikely that an IRB would have the expertise that could be assembled in an OGPBS, particularly that provided by members of the population under consideration. Second, investigators who will collect samples for submission to the repository will come from different institutions, with different IRBs. Greater continuity can be achieved by the ability to coordinate the OGPBS, for example, by having some members participate in several groups. And third, it is expected that oversight will be ongoing during the entire process of sample collection, acquisition by the repository, distribution, and generation of research results. Only a group constituted specifically for this purpose is likely to provide the appropriate level of protection over an extended period of time, and, specifically, beyond the period of review by an IRB, which would end with the collection of the samples.

Some populations might consider these protections inadequate, and some investigators might consider them too onerous. However, the concept behind the OGPBS model is that it provides a flexible approach to maintaining high standards for the protection of diverse populations with different concerns while attempting to provide a valuable genetic resource to the research community. It is hoped that the proposed establishment of OGPBS and the outline of proposed protections will promote discussion of these recommendations or alternatives by the genetics and bioethics communities and by the populations that will be the potential sources of samples and the partners in this valuable research resource.

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Electronic-Database Information

URLs for data in this article are as follows:

Human Genetic Cell Repository, The, http://locus.umdnj.edu/nigms/

Workshop on Population-Based Samples for the NIGMS Human Genetic Cell Repository, http://www.nih.gov/nigms/news/reports/cellrepos.html

Title 45, Code of Federal Regulations, Part 46, http://grants.nih.gov/grants/oprr/humansubjects/45cfr46.htm

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Letter to Human Genetics Journals

To the Editor:

The International Federation of Human Genetics Societies (IFHGS) was founded in 1996. This report was written to inform the international community of human geneticists of the history, purpose, and structure of the organization.

The IFHGS was founded to provide a transparent structure to facilitate communication throughout the international community of human geneticists. The IFHGS, still in its infancy, serves its constituent members—human genetics societies around the world—by providing a platform to share, interactively, information about research, education, and clinical services. The bylaws of the Federation state that "the purpose of The International Federation of Human Genetics Societies (the Federation) is to provide a forum for organized groups dedicated to all aspects of human genetics, including research, clinical practice, and professional and lay education. The Federation will enable communication between its member groups and encourage interaction between workers in genetics fields and in related sciences and will make itself available to promote meetings and publications and other forums which support human genetics research and practice."

The IFHGS presently has two levels of membership: full members and corresponding members. The three founding multinational societies, which are full members, are The American Society of Human Genetics (ASHG), The European Society of Human Genetics (ESHG), and The Human Genetics Society of Australasia (HGSA).

As new multinational or regional societies are formed, they may apply to the IFHGS for full-member status. Two regional societies—the Latin American Society and the East-Asian Society—are candidates for full membership. Representatives of full-member societies constitute the Executive Committee. The representatives' costs for participation in IFHGS activities are borne by the societies that they represent, and, as currently organized, the IFHGS does not require a budget or paid administrative staff.

National human genetics societies are eligible to participate in the IFHGS as corresponding members. All participating individuals, whether from full- or corresponding-member societies, are elected officers or long-term representative appointees of the constituent human genetics societies. Any geneticist in the world who is a member of an affiliated human genetics society is automatically connected to the IFHGS.

The 34 national human genetics societies that are presently corresponding members of the IFHGS are listed in table 1.

At the Ninth International Congress of Human Genetics in Brazil, representatives of the IFHGS met and decided to undertake the organization and support of future international congresses of human genetics. The IFHGS offered to subsume the annual meetings of full-member societies into these congresses so as to guarantee high attendance by avoiding any competition with other annual meetings. This idea was proposed to the leaders of the Permanent Committee of the International Congresses of Human Genetics, which then selected the European Society of Human Genetics as the host of the Tenth International Congress of Human Genetics, which is to be held in Vienna on May 16–19, 2001. Future

Table 1

Corresponding Members of the International Federation of Human Genetics Societies

Name of Society	Representative
American College of Medical Genetics	R. Rodney Howell
Argentina Society of Medical Genetics	Susana Turyk
Austrian Society for Human Genetics	Gerd Utermann
Brazilian Clinical Genetics Society	Joao Monteiro de Pina-Neto
British Society for Human Genetics	Andrew Read
Canadian College of Medical Genetics	Jane Evans
Czech Society of Medical Genetics	Jiri Santavy
Finnish Society of Medical Genetics	Minna Poyhonen
French Society of Human Genetics	Roland Berger
German Society for Human Genetics	Jorg Schmidtke
Hellenic Society of Medical Genetics	Micchael Petersen
Hungarian Society of Human Genetics	Gyorgy Kosztolanyi
Indian Society of Human Genetics	Kiran Kucheria
Irish Society of Human Genetics	Nollaig Parfrey
Israeli Society of Medical Geneticists	Zvi Borochowitz
Italian Society of Human Genetics	Bruno Dallapiccola
Japanese Society of Human Genetics	Keiya Tada
Korean Society of Human Genetics	Ho Suk Saw
Latvian Medical Genetics Society	Rita Lugovska
Lithuanian Society of Human Genetics	Vaidutis Kucinskas
Mexican Association of Human Genetics	Jose Maria Cantu
Netherlands Society of Human Genetics	Gerd-Jan van Ommen
Norwegian Society of Medical Genetics	Trond Leren
Polish Society of Human Genetics	Jerzy Nowak
Portuguese Society of Human Genetics	Carolino Monteiro
Romanian Society of Human Genetics	Covic Mircea
Russian Society of Human Genetics	Evgeny Ginter
Serbian Society for Human Genetics	Miroslava Micic
South African Society for Human Genetics	Arnold Christianson
Spanish Association of Human Genetics	Alberto Valiente
Swedish Society of Human Genetics	Ulf Kristoffersson
Swiss Society of Medical Genetics	Daniel Schorderet
Turkish Association of Medical Genetics	Memnune Apak
Genetics Society of Vietnam	Le Dinh Luong